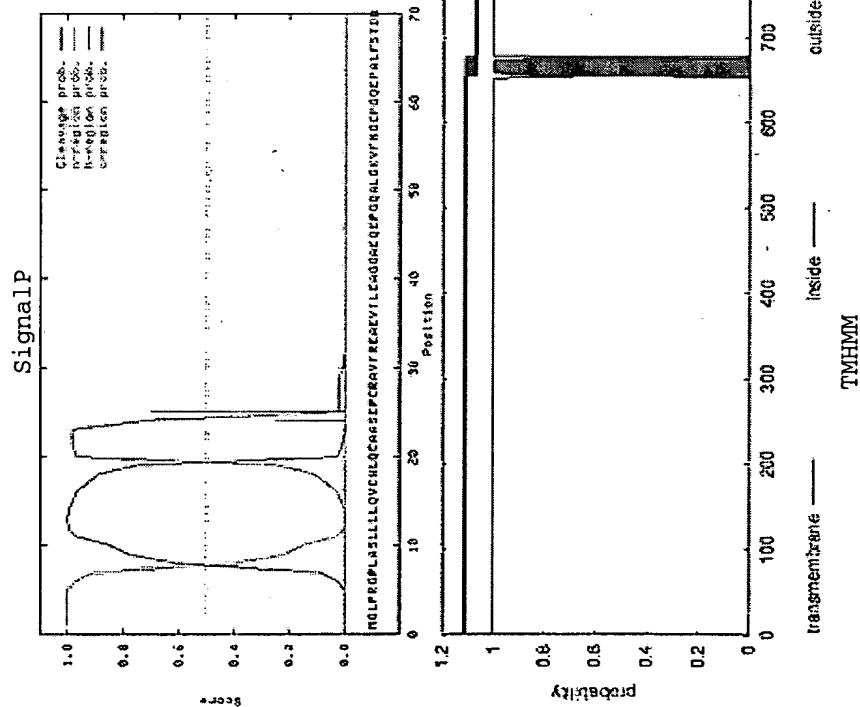


Figure 1

PCTUC5 829 amino acids



RESULTS

signal peptide probability > 99.9%
 maximum cleavage site probability = 70.2%
 number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 24 and 25

MGLPRGPLASLLLLLQVCWLQCAAS ↓ EPCRAVFREA...

Topology

N-terminus external & C-terminus internal

residues 25 - 654 = extracellular

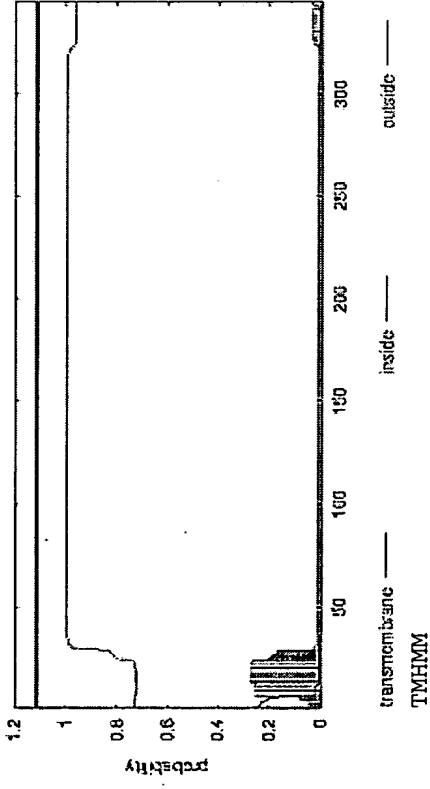
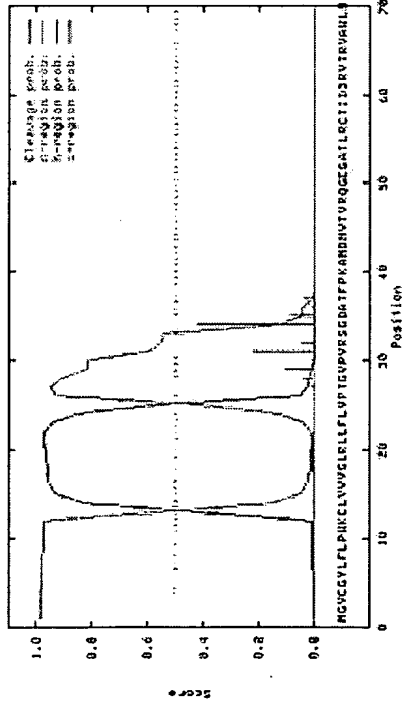
residues 655 - 677 = transmembrane

residues 678 - 829 = intracellular

Figure 2

PCTUC93 345 amino acids

SignalP



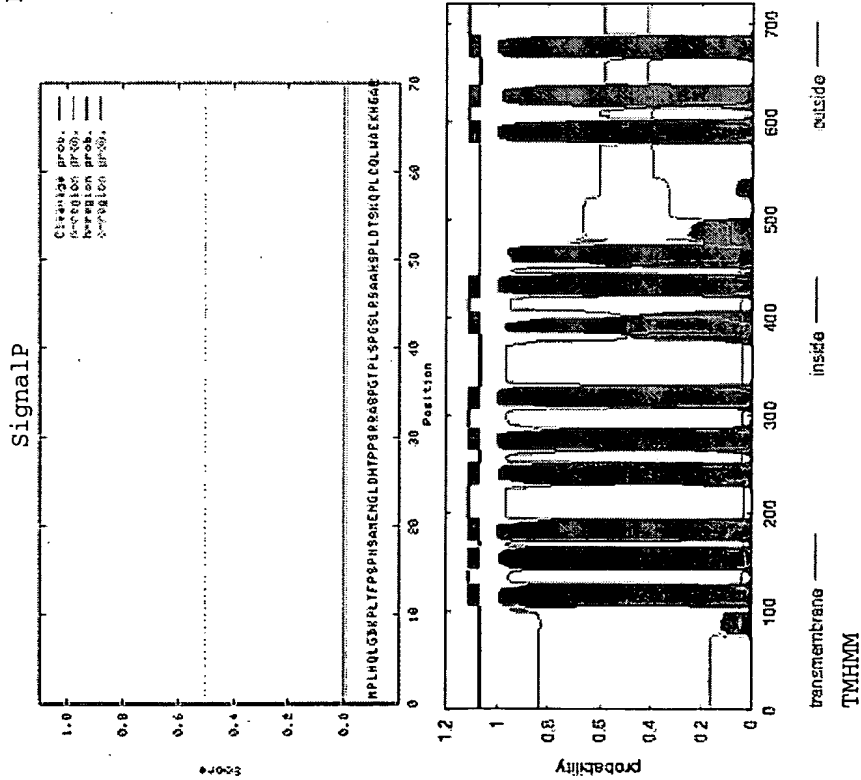
RESULTS
 signal peptide probability = 98.3%
 maximum cleavage site probability = 41.9%
 number of probable transmembrane regions = 0

ANALYSIS
 Cleaved signal peptide
 Cleavage site = between position 33 and 34
 MGVCGYLFLPWKCLVVVSLRLLFLVPTGVPVRS ↓
 GDATFPKAMD...

Topology
 SECRETED
 residues 34 - 345 = extracellular

Figure 3

PCTUC190 722 amino acids



ANALYSIS
N-terminal signal sequence independent membrane insertion
Topology
N-terminus internal & C-terminus external

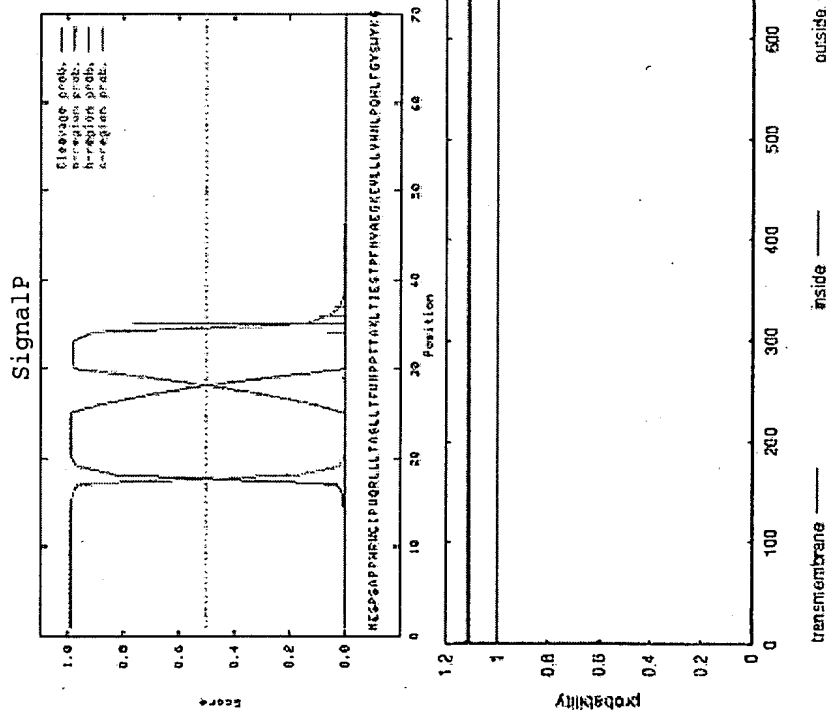
residues 1 - 105 = intracellular
residues 106 - 128 = transmembrane
residues 129 - 142 = extracellular
residues 143 - 165 = transmembrane
residues 166 - 171 = intracellular
residues 172 - 194 = transmembrane
residues 195 - 229 = extracellular
residues 230 - 252 = transmembrane
residues 253 - 264 = intracellular
residues 265 - 287 = transmembrane
residues 288 - 306 = extracellular
residues 307 - 329 = transmembrane
residues 330 - 383 = intracellular
residues 384 - 406 = transmembrane
residues 407 - 420 = extracellular
residues 421 - 443 = transmembrane
residues 444 - 578 = intracellular
residues 579 - 601 = transmembrane
residues 602 - 615 = extracellular
residues 616 - 638 = transmembrane
residues 639 - 666 = intracellular
residues 667 - 689 = transmembrane
residues 690 - 722 = extracellular

RESULTS

signal peptide probability = 0%
signal anchor probability = 0%
number of probable transmembrane regions =

Figure 4

PCTUC239 702 amino acids



ANALYSIS

Cleaved signal peptide

Cleavage site = between position 34 and 35

MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTA ↓

KLTISTPFN...

Topology

SECRETED

residues 35 - 702 = extracellular

TMHMM

RESULTS

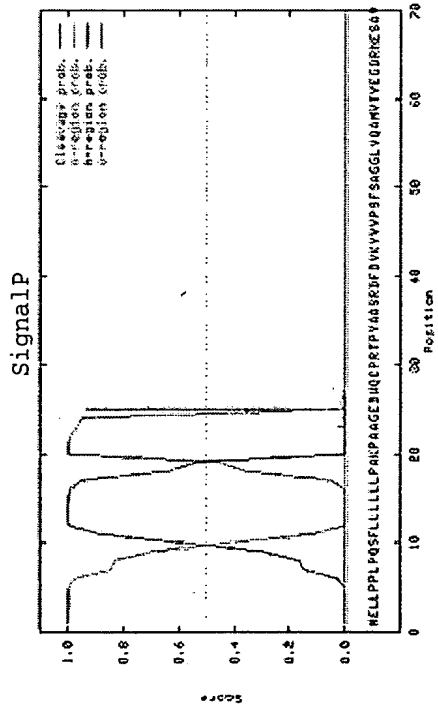
signal peptide probability = 99.3%

maximum cleavage site probability = 76.5%

number of probable transmembrane regions = 0

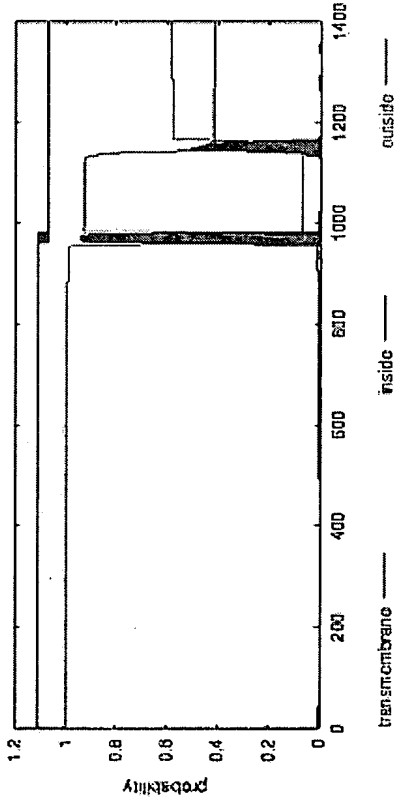
Figure 5

PCTUC246 1400 amino acids



ANALYSIS
 Cleaved signal peptide
 Cleavage site = between position 24 and 25
 MELLPPLPQSFLLLLLLLPAKPAAG ↓ EDWQCPRTPY...

Topology
 N-terminus external & C-terminus internal
 residues 25 - 959 = extracellular
 residues 960 - 982 = transmembrane
 residues 983 -1400 = intracellular

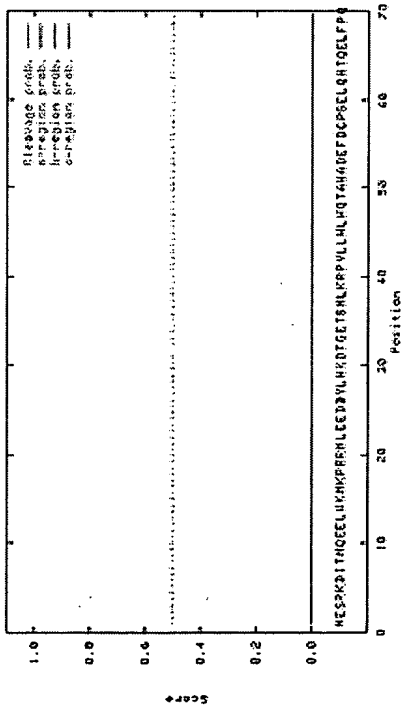


RESULTS
 signal peptide probability > 99.9%
 maximum cleavage site probability = 93.6%
 number of probable transmembrane regions = 1

Figure 6

PCTUC360 339 amino acids

SignalP



RESULTS

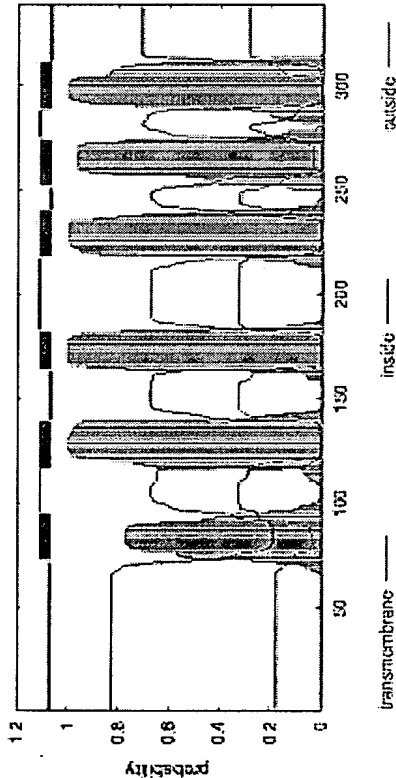
signal peptide probability = 0%
signal anchor probability = 0%
number of probable transmembrane regions = 6

ANALYSIS

N-terminal signal sequence independent membrane insertion
Topology

N-terminus & C-terminus internal

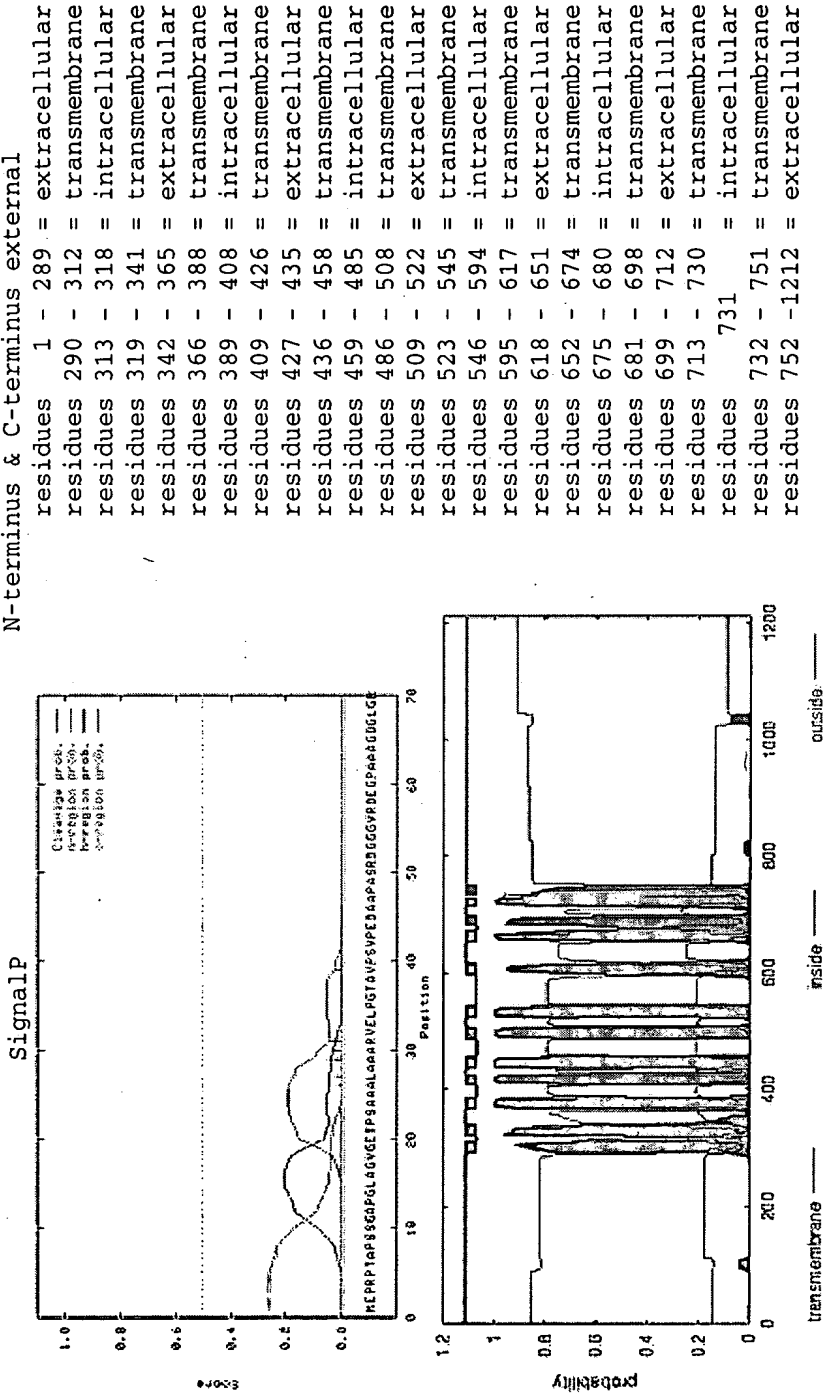
residues 1 - 72 = intracellular
residues 73 - 95 = transmembrane
residues 96 - 116 = extracellular
residues 117 - 139 = transmembrane
residues 140 - 163 = intracellular
residues 164 - 182 = transmembrane
residues 183 - 217 = extracellular
residues 218 - 240 = transmembrane
residues 241 - 251 = intracellular
residues 252 - 274 = transmembrane
residues 275 - 288 = extracellular
residues 289 - 311 = transmembrane
residues 312 - 339 = intracellular



TMHMM

Figure 7

PCTUC462 1212 amino acids



TMHMM

RESULTS

signal peptide probability = 25.9%

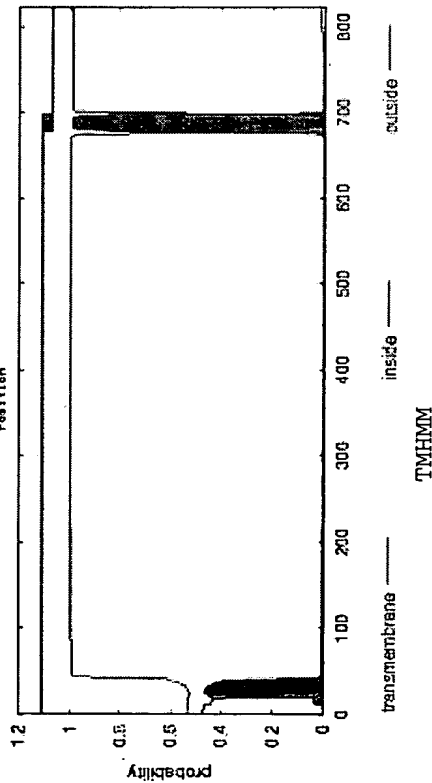
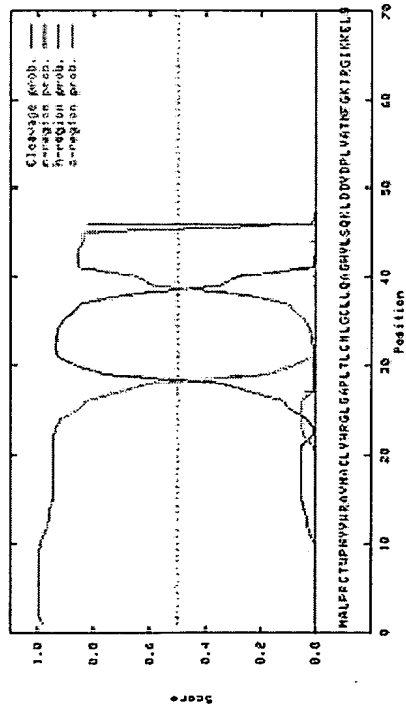
signal anchor probability = 0%

number of probable transmembrane regions =

Figure 8

PCTUC468 823 amino acids

SignalP



RESULTS

signal peptide probability = 98.4%
 maximum cleavage site probability = 82.2%
 number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 45 and 46

MALPRCTWPNYVVRVAVMACLVHRGLGAPLTLCMLGCLLQAGHVLS ↓
 QKLDDVDPLV...

Topology

N-terminus external & C-terminus internal

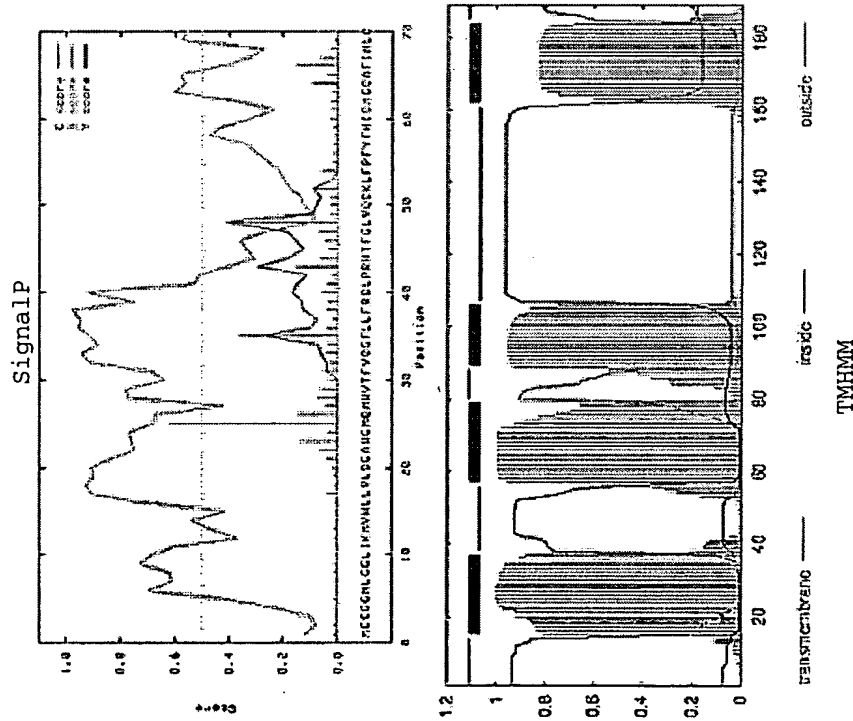
residues 46 - 676 = extracellular

residues 677 - 699 = transmembrane

residues 700 - 823 = intracellular

Figure 9

PCTUC536 189 amino acids



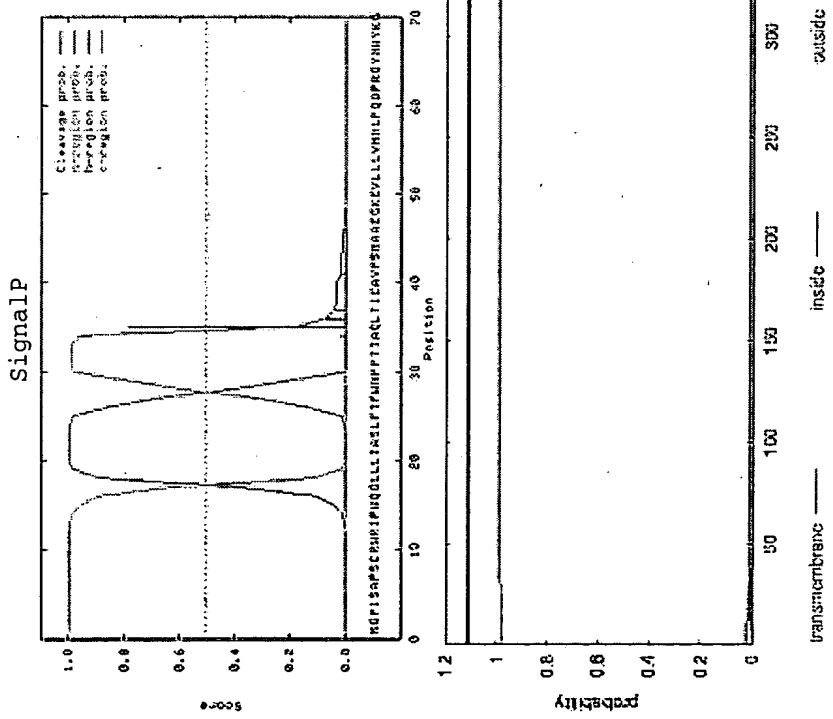
ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology

N-terminus & C-terminus external
residues 1 - 14 = extracellular
residues 15 - 37 = transmembrane
residues 38 - 56 = intracellular
residues 57 - 79 = transmembrane
residues 80 - 88 = extracellular
residues 89 - 106 = transmembrane
residues 107 - 161 = intracellular
residues 162 - 184 = transmembrane
residues 185 - 189 = extracellular

RESULTS
signal peptide probability = 29.2%
signal anchor probability = 37.2%
number of probable transmembrane regions = 4

Figure 10

PCTUC582 349 amino acids



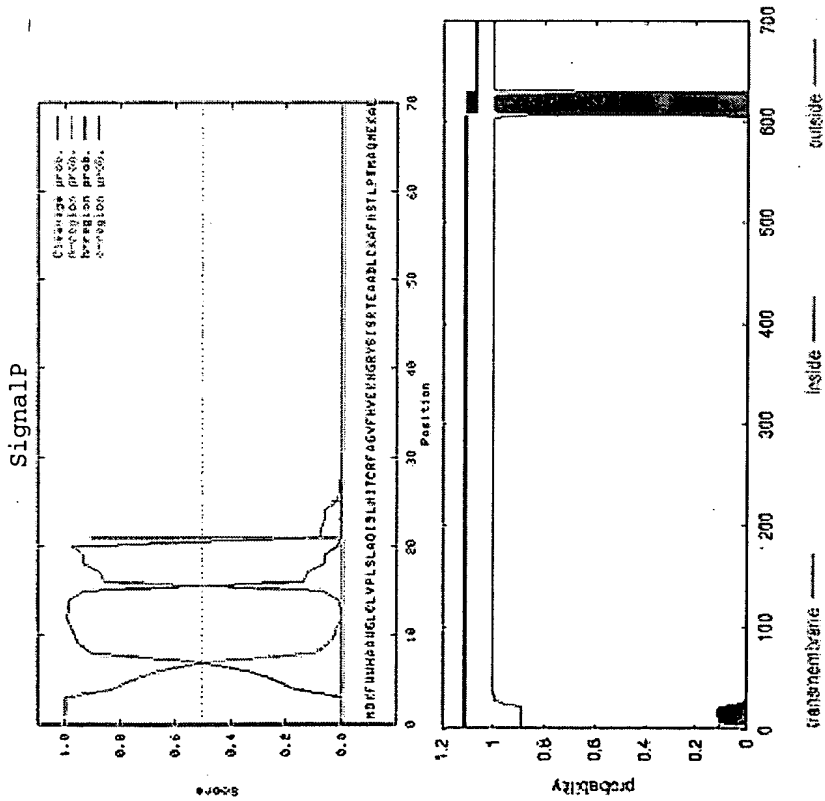
ANALYSIS
Cleaved signal peptide
Cleavage site = between position 34 and 35
MGPI SAPSCRWRIPWQGLLLTASLFTFWNPPTTA ↓
QLTIEAVPSN...
Topology
SECRETED
residues 35 - 349 = extracellular

RESULTS
signal peptide probability = 99.3%
maximum cleavage site probability = 78.6%
number of probable transmembrane regions = 0

Figure 11

PCTUC605 699 amino acids

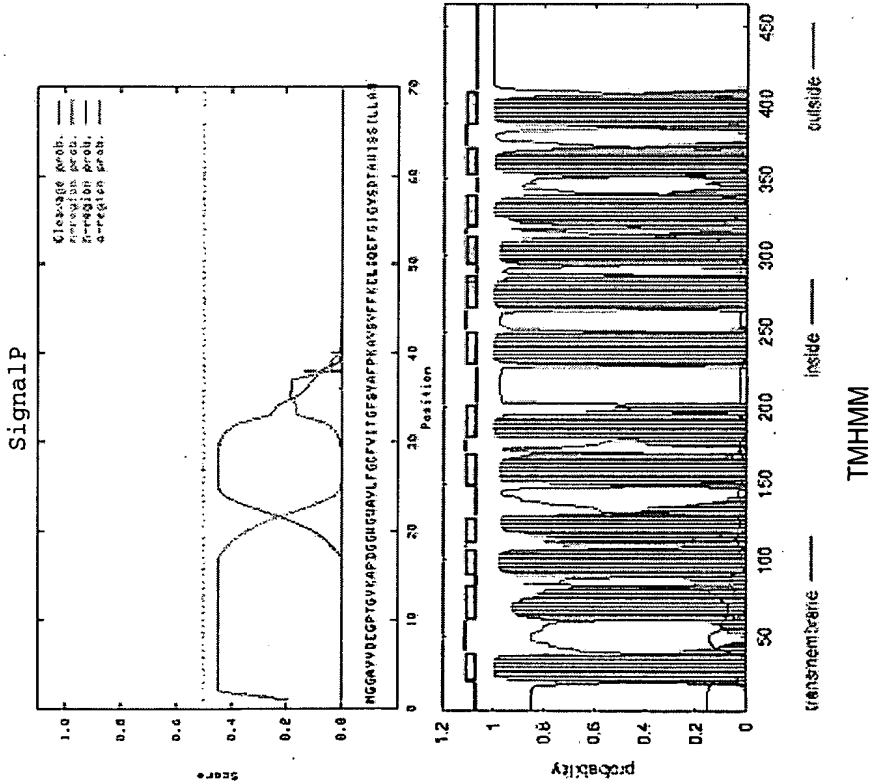
ANALYSIS
 Cleaved signal peptide
 Cleavage site = between position 20 and 21
 MDKFWWFAAWGLCLVPLSLA ↓ QIDLNITCRF...
 Topology
 N-terminus external & C-terminus internal
 residues 21 - 606 = extracellular
 residues 607 - 629 = transmembrane
 residues 630 - 699 = intracellular



RESULTS
 signal peptide probability = 99.7%
 maximum cleavage site probability = 90.9%
 number of probable transmembrane regions = 1

Figure 12

PCTUC629 465 amino acids



ANALYSIS
N-terminal signal sequence independent membrane insertion
Topology
N-terminus & C-terminus internal

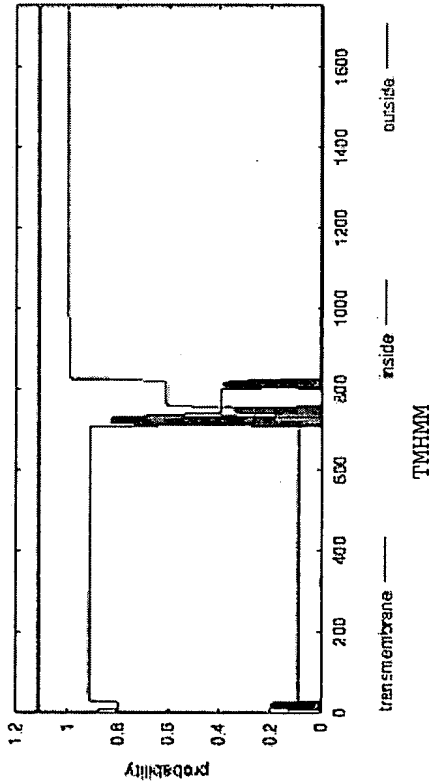
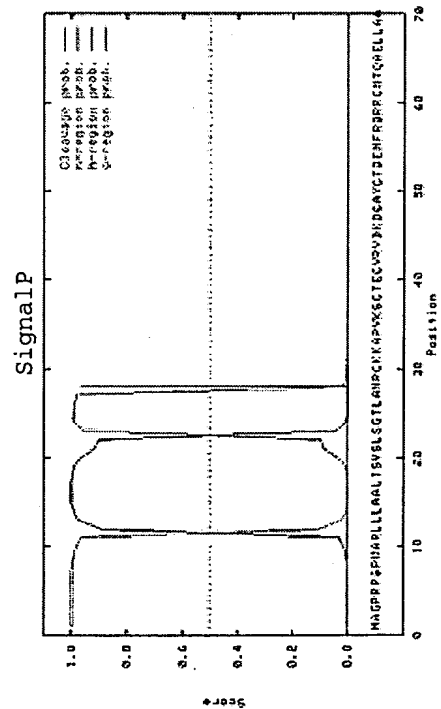
residues 1 - 19 = intracellular
residues 20 - 39 = transmembrane
residues 40 - 60 = extracellular
residues 61 - 83 = transmembrane
residues 84 - 89 = intracellular
residues 90 - 107 = transmembrane
residues 108 - 110 = extracellular
residues 111 - 128 = transmembrane
residues 129 - 147 = intracellular
residues 148 - 170 = transmembrane
residues 171 - 179 = extracellular
residues 180 - 202 = transmembrane
residues 203 - 227 = intracellular
residues 228 - 250 = transmembrane
residues 251 - 264 = extracellular
residues 265 - 287 = transmembrane
residues 288 - 293 = intracellular
residues 294 - 313 = transmembrane
residues 314 - 317 = extracellular
residues 318 - 340 = transmembrane
residues 341 - 351 = intracellular
residues 352 - 371 = transmembrane
residues 372 - 385 = extracellular
residues 386 - 408 = transmembrane
residues 409 - 465 = intracellular

RESULTS
signal peptide probability = 19.3%
signal anchor probability = 25.6%
number of probable transmembrane regions = 12

Figure 13

PCTUC722 1752 amino acids

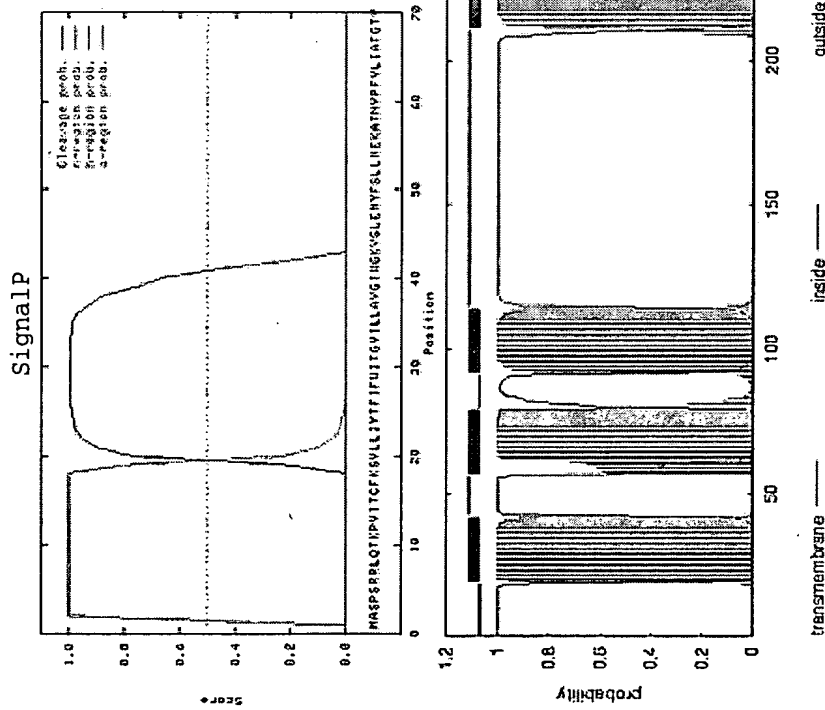
ANALYSIS
Cleaved signal peptide
Cleavage site = between position 27 and 28
MAGPRPSPWARLLLAALISVLSGTLA ↓ NRCKKAPVKS...
Topology
SECRETED
residues 28 - 1752 = extracellular



RESULTS
signal peptide probability > 99.9%
maximum cleavage site probability = 96.8%
number of probable transmembrane regions = 0

Figure 14

PCTUC748 245 amino acids



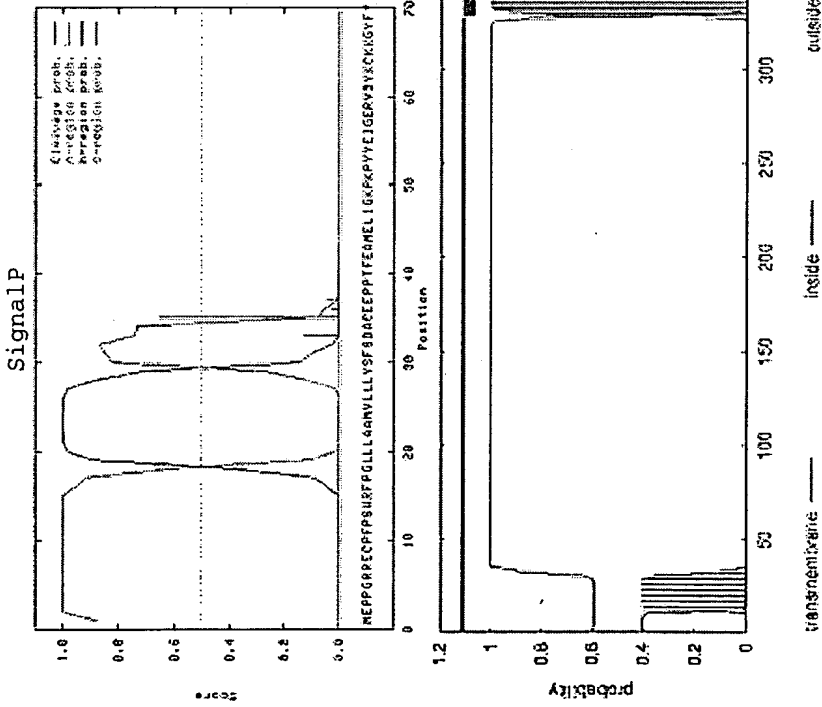
ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology

N-terminus & C-terminus internal
residues 1 - 19 = intracellular
residues 20 - 42 = transmembrane
residues 43 - 56 = extracellular
residues 57 - 79 = transmembrane
residues 80 - 91 = intracellular
residues 92 - 114 = transmembrane
residues 115 - 210 = extracellular
residues 211 - 233 = transmembrane
residues 234 - 245 = intracellular

RESULTS
signal peptide probability = 0.3%
signal anchor probability = 99.7%
number of probable transmembrane regions = 4

Figure 15

PCTUC784 377 amino acids



TMHMM

RESULTS

signal peptide probability = 87.0%
maximum cleavage site probability = 65.3%
number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 34 and 35

MEPPGRRRECPFPSSWRFPGLLLAAMVLLLYSFSDA ↓
CEEPTFEAM...

Topology

N-terminus external & C-terminus internal

residues 35 - 328 = extracellular

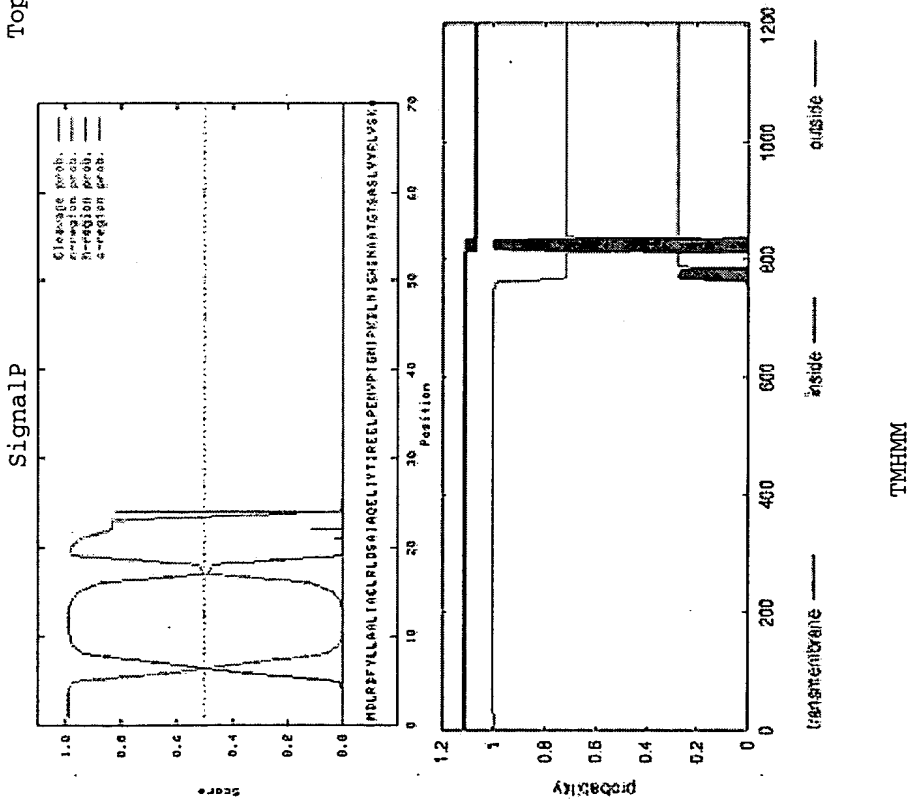
residues 329 - 351 = transmembrane

residues 352 - 377 = intracellular

Figure 16

PCTUC812 1203 amino acids

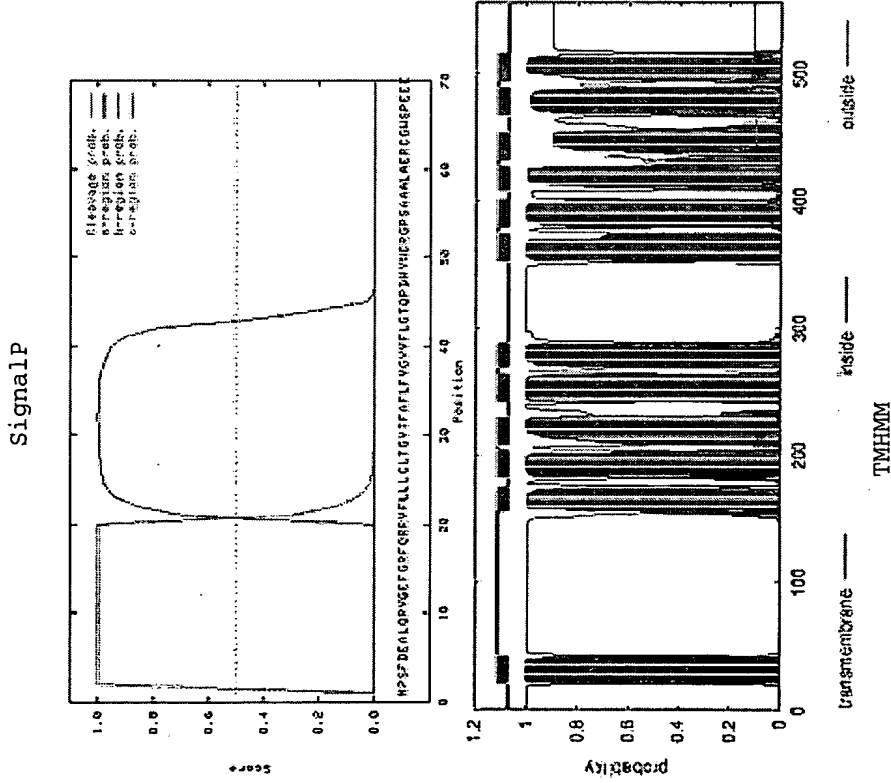
ANALYSIS
Cleaved signal peptide
Cleavage site = between position 23 and 24
MDLRDFYLLAALIACLRLDSAIA ↓ QELIYTIREE...
Topology
N-terminus external & C-terminus internal
residues 25 - 813 = extracellular
residues 814 - 836 = transmembrane
residues 837 - 1203 = intracellular



RESULTS
signal peptide probability = 99.1%
maximum cleavage site probability = 82.5%
number of probable transmembrane regions = 1

Figure 17

PCTUC856 556 amino acids



ANALYSIS

Signal Anchor (non-cleaved signal peptide)
Topology

N-terminus & C-terminus internal

residues 1 - 20 = intracellular
residues 21 - 43 = transmembrane
residues 44 - 155 = extracellular
residues 156 - 175 = transmembrane
residues 176 - 181 = intracellular
residues 182 - 204 = transmembrane
residues 205 - 207 = extracellular
residues 208 - 230 = transmembrane
residues 231 - 241 = intracellular
residues 242 - 264 = transmembrane
residues 265 - 268 = extracellular
residues 269 - 288 = transmembrane
residues 289 - 351 = intracellular
residues 352 - 374 = transmembrane
residues 375 - 378 = extracellular
residues 379 - 401 = transmembrane
residues 402 - 407 = intracellular
residues 408 - 427 = transmembrane
residues 428 - 431 = extracellular
residues 432 - 454 = transmembrane
residues 455 - 466 = intracellular
residues 467 - 489 = transmembrane
residues 490 - 493 = extracellular
residues 494 - 516 = transmembrane
residues 517 - 556 = intracellular

RESULTS

signal peptide probability = 0.1%

signal anchor probability = 99.9%

number of probable transmembrane regions = 12

Figure 18

PCTUC898

807 amino acids

RESULTS
signal peptide probability = 0%
signal anchor probability = 48.6%
number of probable transmembrane regions = 10

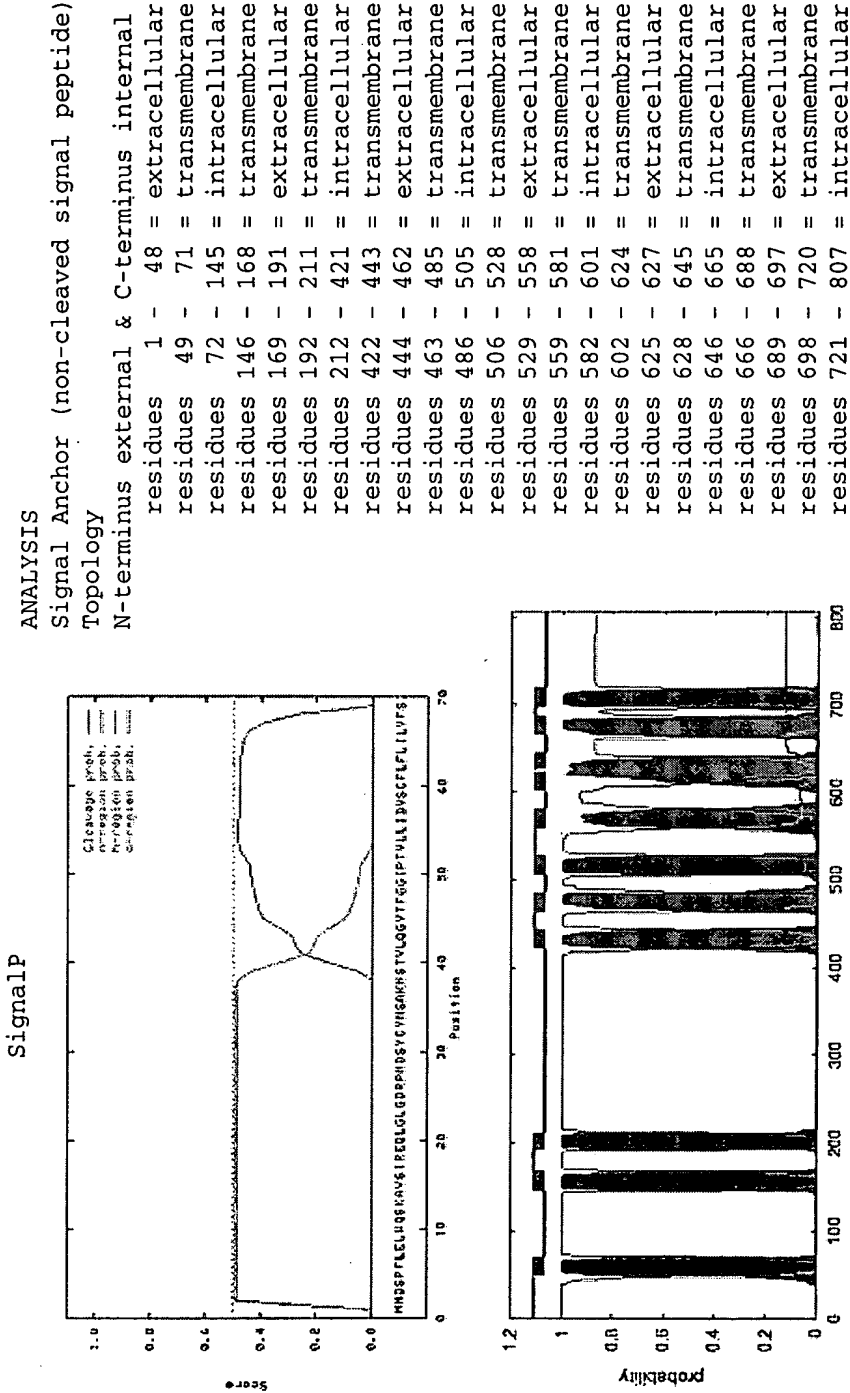
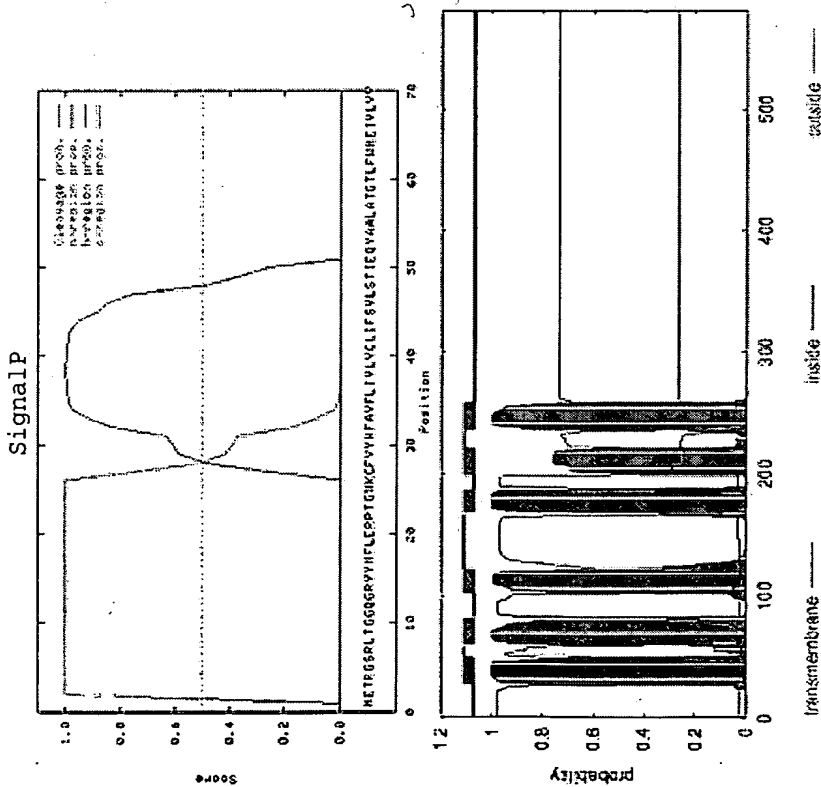


Figure 19

PCTUC935 581 amino acids

ANALYSIS
Signal Anchor (non-cleaved signal peptide)
Topology
N-terminus & C-terminus internal
residues 1 - 27 = intracellular
residues 28 - 50 = transmembrane
residues 51 - 59 = extracellular
residues 60 - 82 = transmembrane
residues 83 - 102 = intracellular
residues 103 - 122 = transmembrane
residues 123 - 167 = extracellular
residues 168 - 187 = transmembrane
residues 222 - 235 = extracellular
residues 188 - 198 = intracellular
residues 236 - 258 = transmembrane
residues 199 - 221 = transmembrane
residues 259 - 581 = intracellular



RESULTS

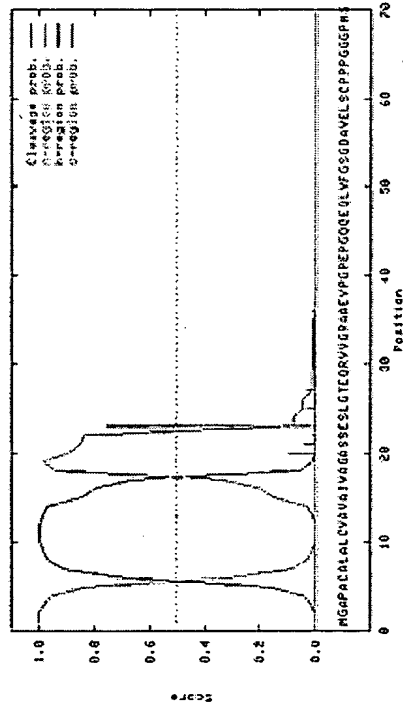
signal peptide probability = 0.02%
signal anchor probability = 99.8%
number of probable transmembrane regions = 6

Figure 20

PCTUC936

806 amino acids

SignalP



RESULTS
 signal peptide probability > 99.9%
 maximum cleavage site probability = 75.4%
 number of probable transmembrane regions = 2
 EXPERIMENTAL EVIDENCE SUPPORTS ONLY TM#1 REGION

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 22 and 23

MGAPACALALCVAVAIAGASS ↓ ESLGTEQRVV...

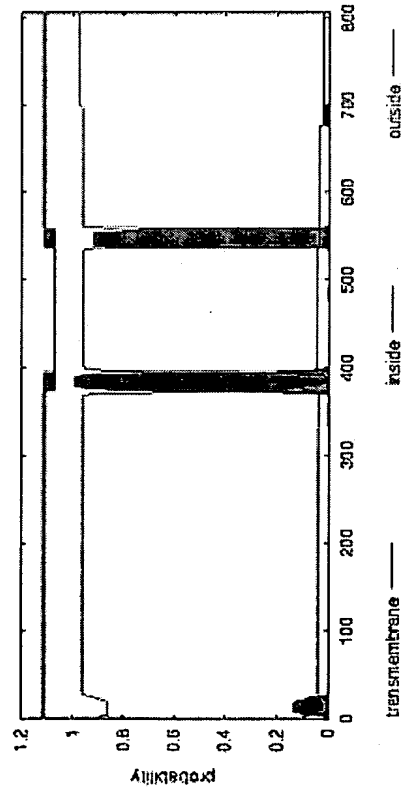
Topology

N-terminus external & C-terminus internal

residues 24 - 372 = extracellular

residues 373 - 395 = transmembrane

residues 396 - 806 = intracellular

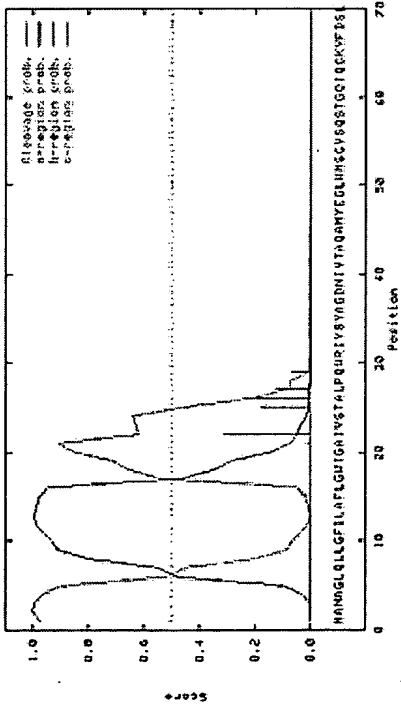


TMHMM

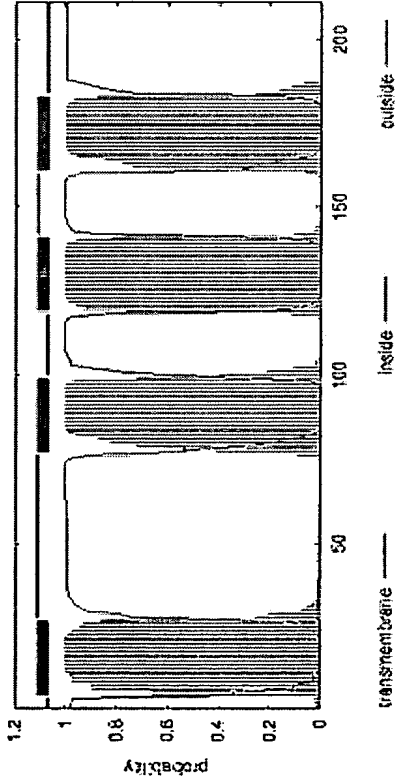
Figure 21

PCTUC986 211 amino acids

SignalP



ANALYSIS
Cleaved signal peptide
Cleavage site = between position 21 and 22
MANAGLQLLGFIILAFILGWIGA ↓ IVSTALPQWR...
Topology
N-terminus external & C-terminus internal
residues 23 - 76 = extracellular
residues 77 - 99 = transmembrane
residues 100 - 118 = intracellular
residues 119 - 141 = transmembrane
residues 142 - 160 = extracellular
residues 161 - 183 = transmembrane
residues 184 - 211 = intracellular

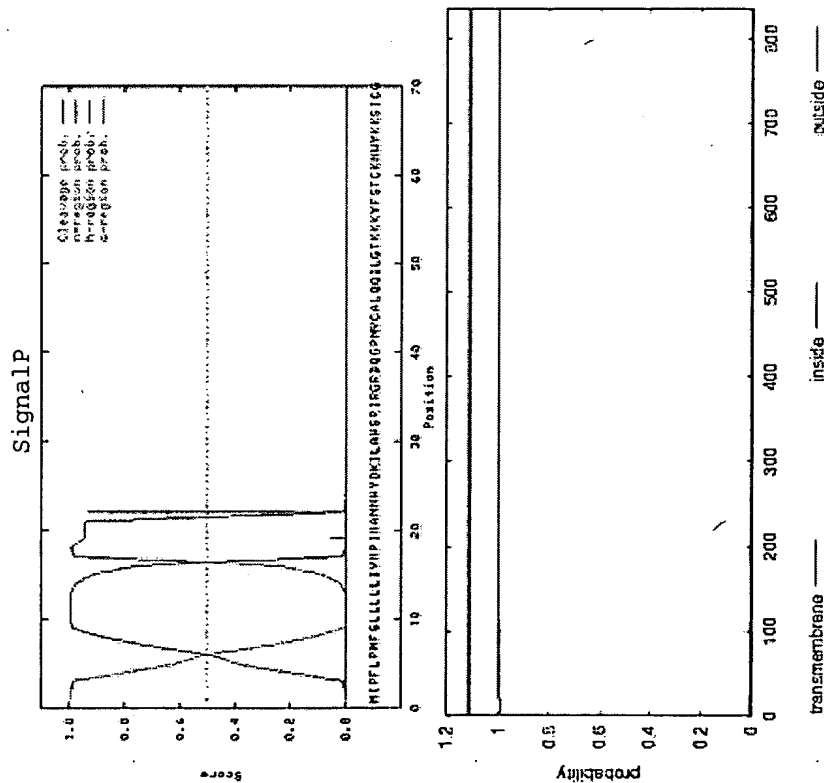


signal peptide probability = 97.6%
maximum cleavage site probability = 31.4%
number of probable transmembrane regions = 4
(#1 cleaved)

Figure 22

PCTUC991 836 amino acids

ANALYSIS
 Cleaved signal peptide
 Cleavage site = between position 21 and 22
 MIPFLPMFSLLLLLLIIVNPINA ↓ NNHYDKILAH...
 Topology
 SECRETED
 residues 22 - 836 = extracellular



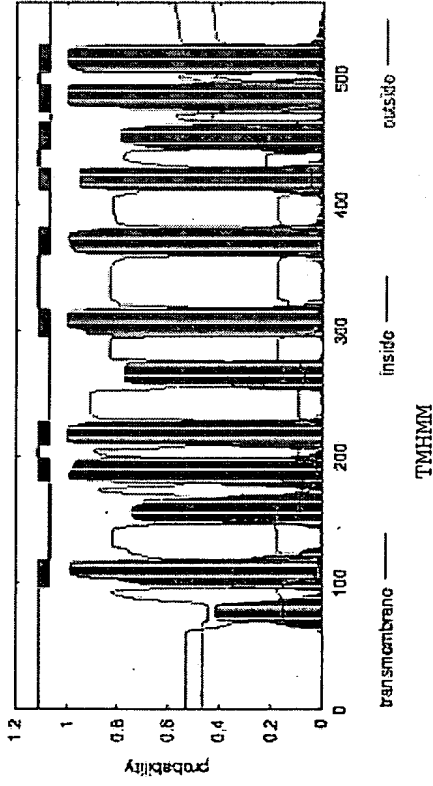
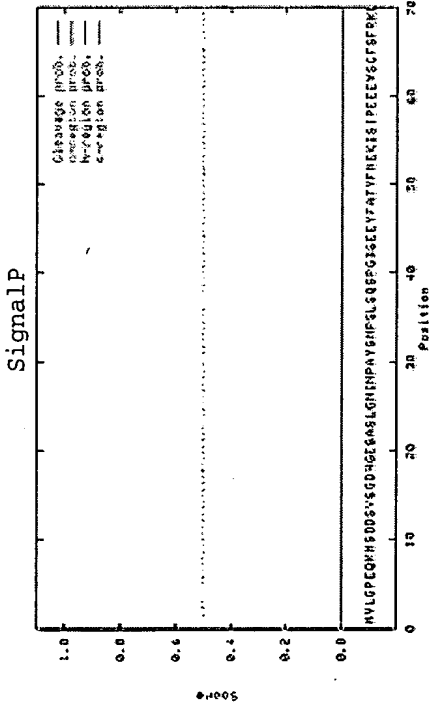
TMHMM

RESULTS

signal peptide probability = 99.9%
 maximum cleavage site probability = 93.4%
 number of probable transmembrane regions = 0

Figure 23

PCTUC992 561 amino acids



RESULTS

signal peptide probability = 0%

signal anchor probability = 0%

number of probable transmembrane regions = 9

ANALYSIS

N-terminal signal sequence independent membrane insertion

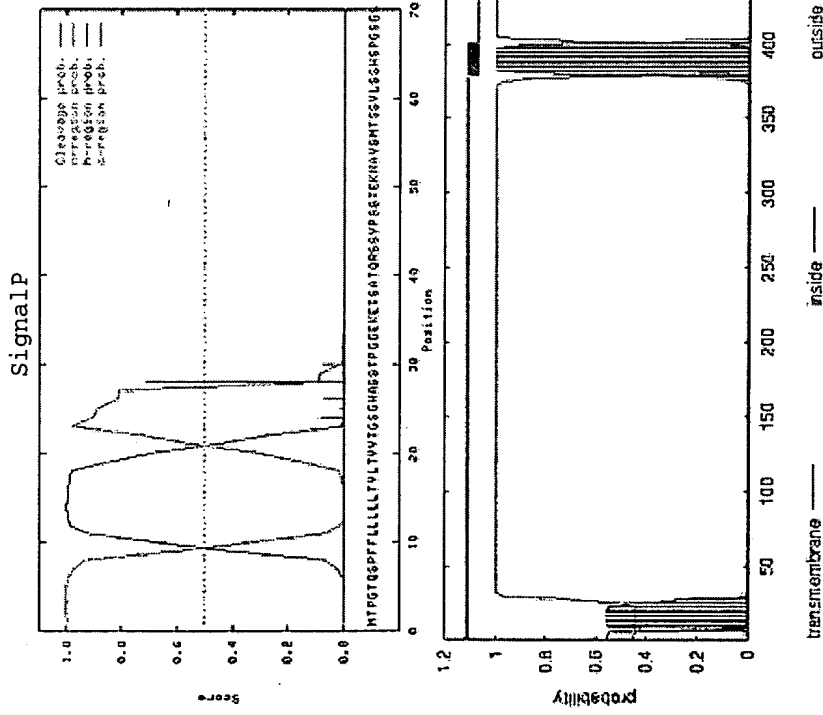
Topology

N-terminus external & C-terminus internal

residues 1 - 95 = extracellular
residues 96 - 118 = transmembrane
residues 119 - 179 = intracellular
residues 180 - 199 = transmembrane
residues 200 - 208 = extracellular
residues 209 - 228 = transmembrane
residues 229 - 294 = intracellular
residues 295 - 317 = transmembrane
residues 318 - 359 = extracellular
residues 360 - 382 = transmembrane
residues 383 - 411 = intracellular
residues 412 - 429 = transmembrane
residues 430 - 443 = extracellular
residues 444 - 466 = transmembrane
residues 467 - 472 = intracellular
residues 473 - 495 = transmembrane
residues 496 - 504 = extracellular
residues 505 - 527 = transmembrane
residues 528 - 561 = intracellular

Figure 24

PCTUC1054 475 amino acids



TMHMM

RESULTS

signal peptide probability = 99.8%
 maximum cleavage site probability = 71.4%
 number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 27 and 28

MTPGTQSPFFLLLLLTVLTVVTGSGHA ↓ SSTPGGEKET...

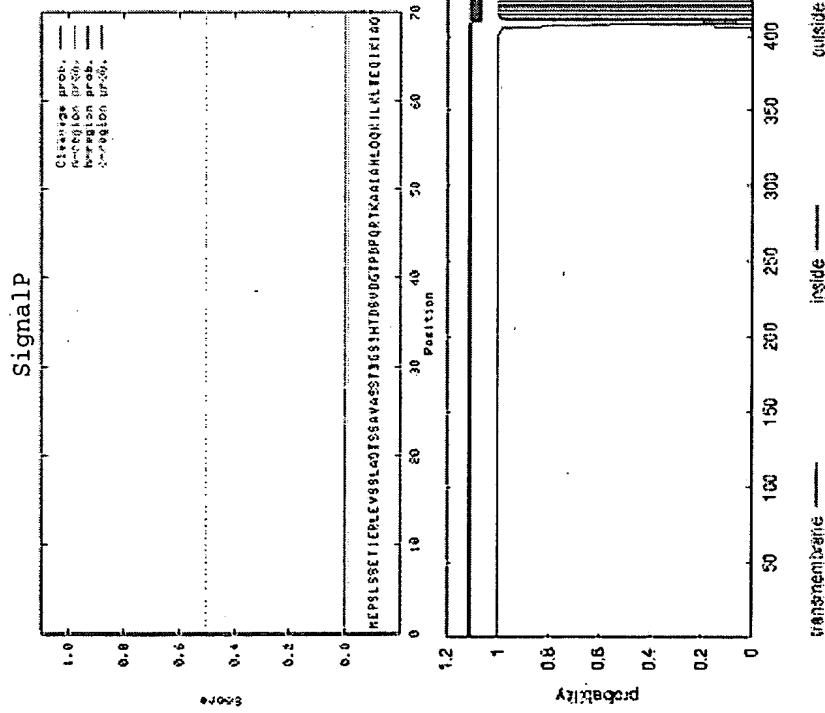
Topology

N-terminus external & C-terminus internal
 residues 28 - 378 = extracellular
 residues 379 - 401 = transmembrane
 residues 402 - 475 = intracellular

Figure 25

PCTUC1061 470 amino acids

ANALYSIS
N-terminal signal sequence independent membrane insertion
Topology
N-terminus & C-terminus external
residues 1 - 408 = extracellular
residues 409 - 431 = transmembrane
residues 432 - 437 = intracellular
residues 438 - 455 = transmembrane
residues 456 - 470 = extracellular

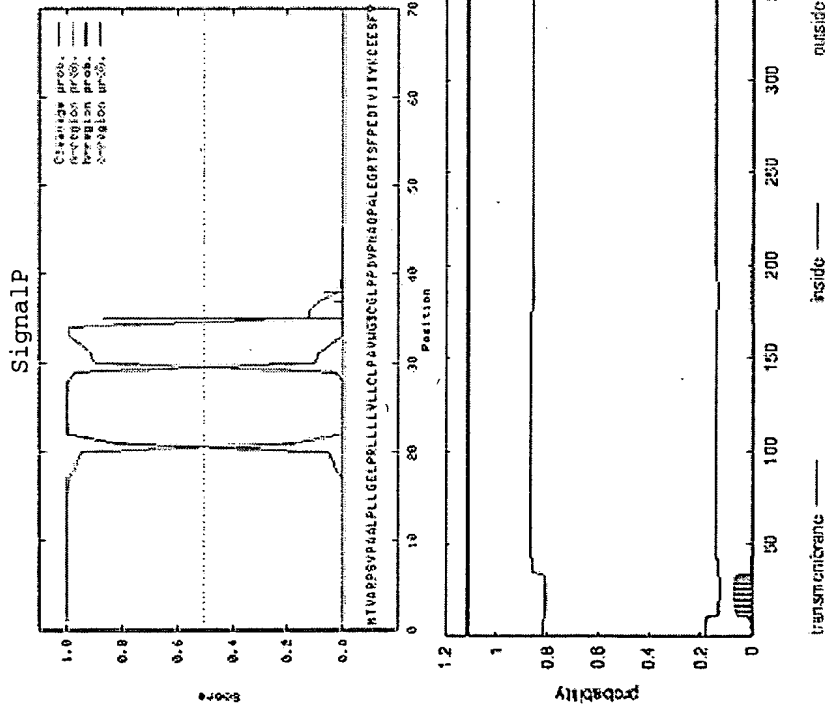


RESULTS

signal peptide probability = 0.6%
signal anchor probability = 0.1%
number of probable transmembrane regions = 2

Figure 26

PCTUC1073 381 amino acids

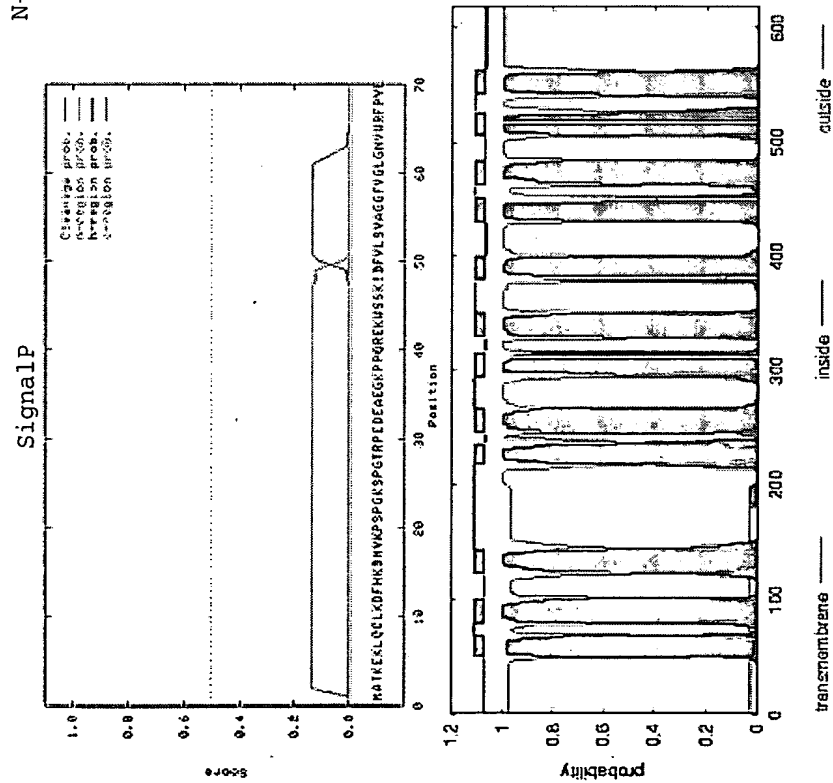


ANALYSIS
Cleared signal peptide
Cleavage site = between position 34 and 35
MTVARPSVPAAALPLLGLPRLLLVLLCLPAVWG ↓
DCGLPPDPVN...
Topology
SECRETED
residues 35 - 381 = extracellular

RESULTS
signal peptide probability > 99.9%
maximum cleavage site probability = 86.9%
number of probable transmembrane regions = 0

Figure 27

PCTUC1075 619 amino acids



RESULTS

signal peptide probability = 0%

signal anchor probability = 13.9%

number of probable transmembrane regions = 12

ANALYSIS

N-terminal signal sequence independent membrane insertion

Topology

N-terminus & C-terminus internal

residues 1 - 49 = intracellular

residues 50 - 69 = transmembrane

residues 70 - 78 = extracellular

residues 79 - 101 = transmembrane

residues 102 - 121 = intracellular

residues 122 - 144 = transmembrane

residues 145 - 217 = extracellular

residues 218 - 236 = transmembrane

residues 237 - 244 = intracellular

residues 245 - 267 = transmembrane

residues 268 - 293 = extracellular

residues 294 - 316 = transmembrane

residues 317 - 328 = intracellular

residues 329 - 351 = transmembrane

residues 352 - 377 = extracellular

residues 378 - 400 = transmembrane

residues 401 - 429 = intracellular

residues 430 - 452 = transmembrane

residues 453 - 461 = extracellular

residues 462 - 484 = transmembrane

residues 485 - 504 = intracellular

residues 505 - 527 = transmembrane

residues 528 - 541 = extracellular

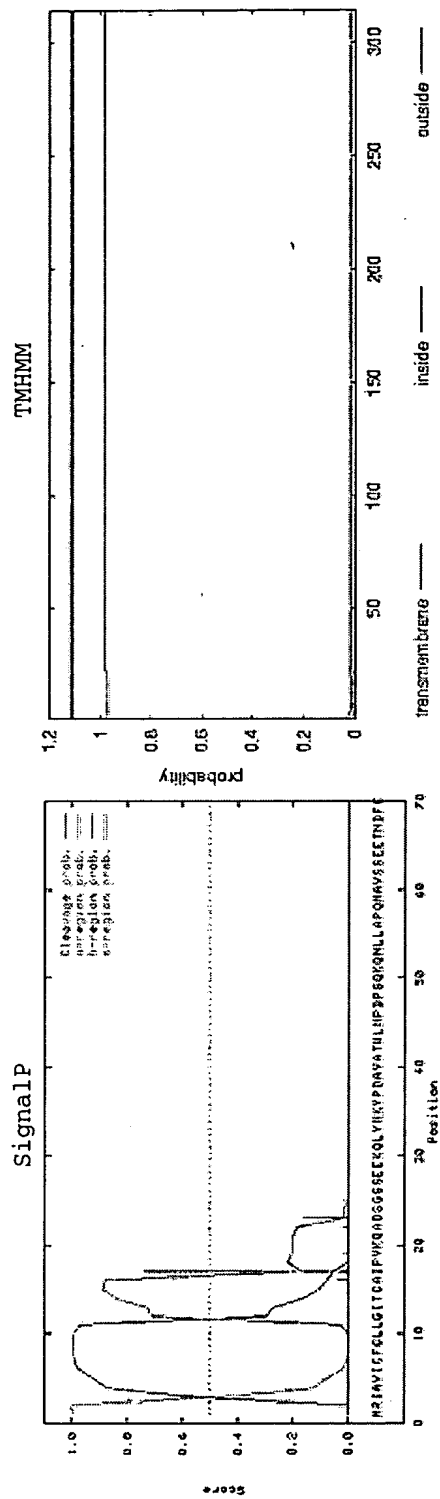
residues 542 - 564 = transmembrane

residues 565 - 619 = intracellular

Figure 28

PCTUC1078

314 amino acids



RESULTS

signal peptide probability = 99.9%
 maximum cleavage site probability = 73.6%
 number of probable transmembrane regions = 0

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 16 and 17

MRIAVICFLLGITCA ↓ IPVKQADSGS...

Topology

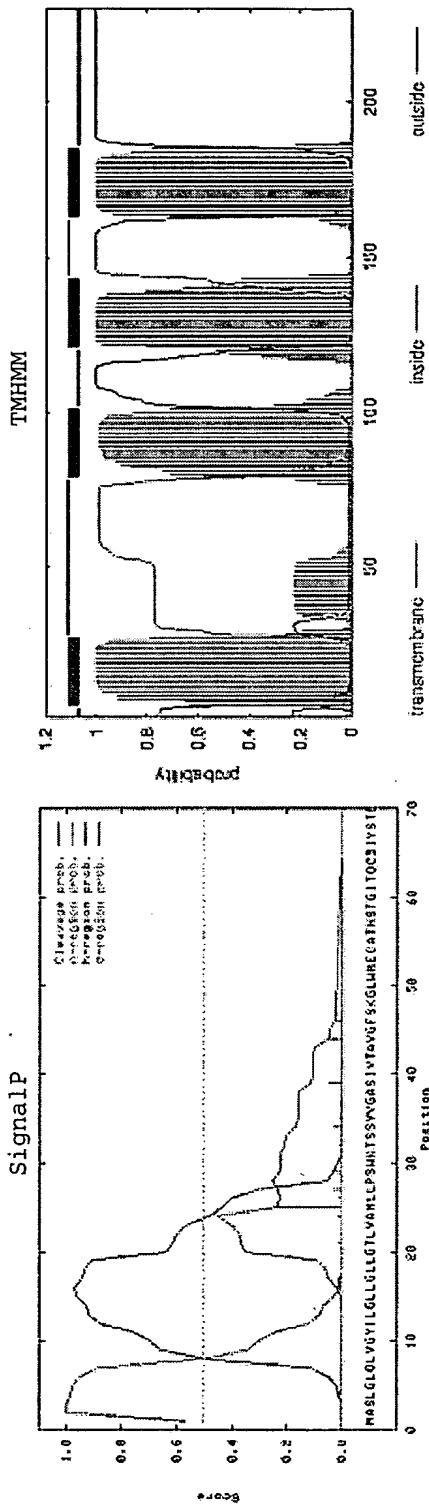
SECRETED

residues 18 - 314 = extracellular

Figure 29

PCTUC1082

230 amino acids



signal peptide probability = 57.0%
maximum cleavage site probability = 23.7%
number of probable transmembrane regions = 4 (#1 cleaved)

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 24 and 25

MASLGQLVGYILGLLGLTVA ↓ MLLPSWKTSS...

Topology

N-terminus external & C-terminus internal

residues 25 - 78 = extracellular

residues 79 - 101 = transmembrane

residues 102 - 120 = intracellular

residues 121 - 143 = transmembrane

residues 144 - 162 = extracellular

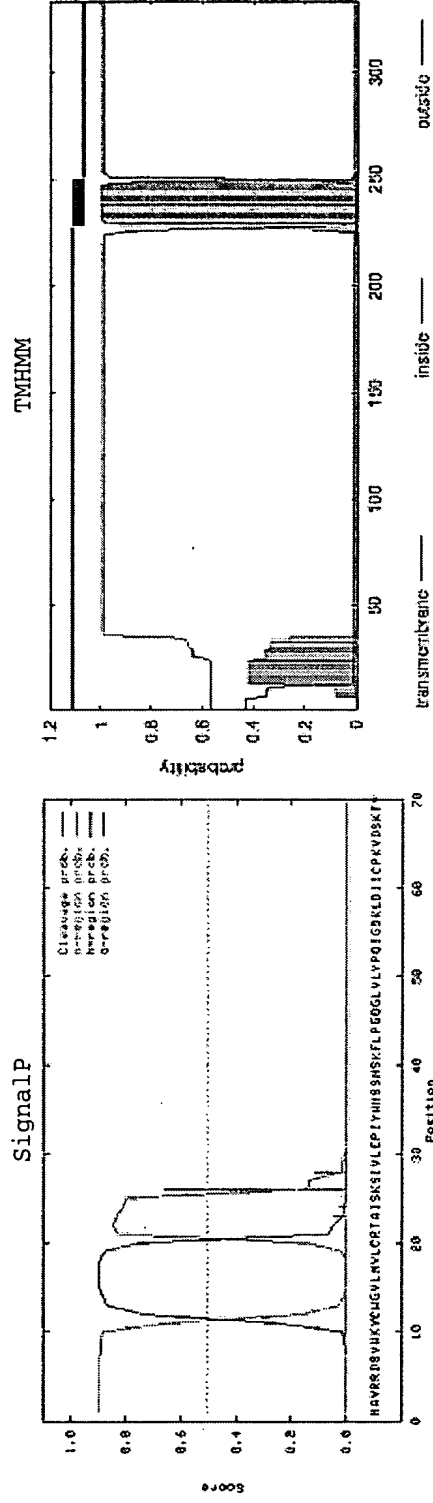
residues 163 - 185 = transmembrane

residues 186 - 230 = intracellular

Figure 30

PCTUC1122

333 amino acids



RESULTS

signal peptide probability = 89.5%
 maximum cleavage site probability = 65.9%
 number of probable transmembrane regions = 1

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 25 and 26

MAVRDSDVWKYCWGVLMLCRTAIS ↓ KSIVLEPIYW...

Topology

N-terminus external & C-terminus internal

residues 26 - 227 = extracellular

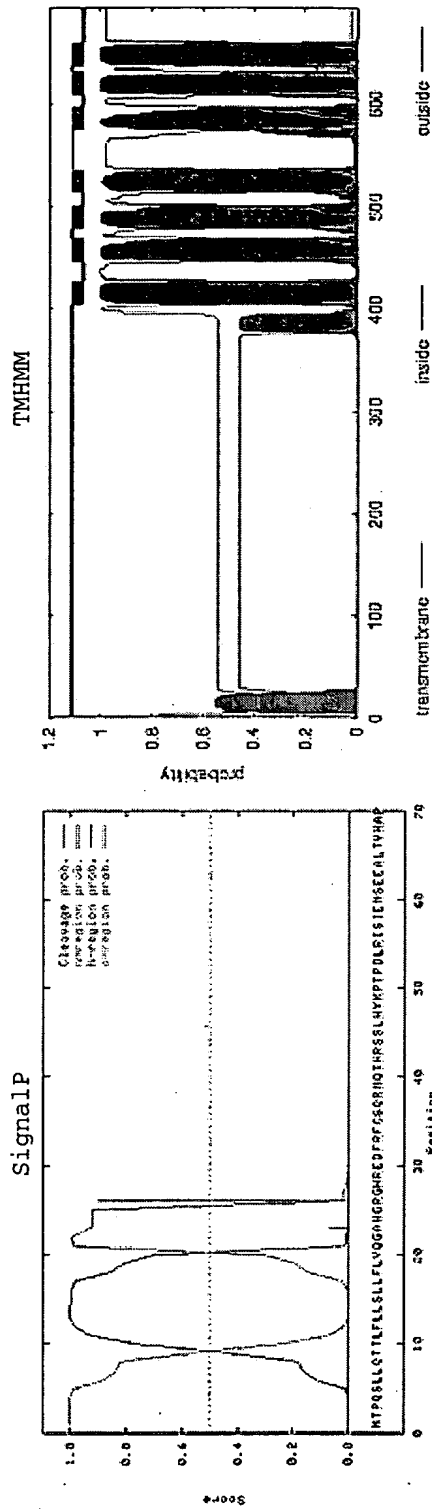
residues 228 - 250 = transmembrane

residues 251 - 333 = intracellular

Figure 31

PCTUC250

693 amino acids



RESULTS

signal peptide probability > 99.9%
 maximum cleavage site probability = 90.4%
 number of probable transmembrane regions = 7

ANALYSIS

Cleaved signal peptide

Cleavage site = between position 25 and 26

MT PQSL LQT TLF LL SLL FLV QGAHG ↓ RGHRED FRFC

Topology

N-terminus external & C-terminus internal

residues 26 - 404 = extracellular

residues 405 - 427 = transmembrane

residues 428 - 446 = intracellular

residues 447 - 469 = transmembrane

residues 470 - 478 = extracellular

residues 479 - 501 = transmembrane

residues 502 - 513 = intracellular

residues 514 - 536 = transmembrane

residues 537 - 574 = extracellular

residues 575 - 597 = transmembrane

residues 598 - 608 = intracellular

residues 609 - 631 = transmembrane

residues 632 - 636 = extracellular

residues 637 - 659 = transmembrane

residues 660 - 693 = intracellular